

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTAACTCCGGTAAGTACCTAGCCCACATGATT
TGA CTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATT CAGGGGCTCTCAAGAACAATGGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTCTTTTCC
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATT CAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTT CAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATT CACGTGT CAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTT CAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTGTAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAATCCTGGGCTTAAG
TGATCTGCCC GCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
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CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
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CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTTCATACTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 202

FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTCA
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC
TCAGCCTCCCAGATAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCCGAGGAAAATGACTCCCCAG
TCGCTGCTGCAGACGACACTGTTCTCTGCTGAGTCTGCTCTTCCCTGGTCCAAGGTGCCACAGGAGGGGCCACAGG
GAAGACTTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG
CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTTCCCTGCAGCCCCACCTGCTTCCCGA
TCCTTCCCTGACCCCAGGGGCCCTTACCACCTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC
TATGGCAAGCGTGAATCTTGTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC
GCCAGCTTACCTTCTCCTTCCACAGTCCCTCCCCACAGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC
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GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTTTCGAG
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CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC
CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTCC
AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAGTAGCCAACCTCAGGAGCCCGTG
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TTTGCTTCTGGCACCTTCCAGCTTGTGCTCTTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCTCTATC
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AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCATGTGATGAAG
CAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCCAGCCGAGACT
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GTTGCTCTGTCTCTCGTGGTCAACCTGAGGGCACTCTGCATCCTCTGTCAATTTAACCCTCAGGTGGCACCCAGGG
CGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC
AGCTCGCCTACCTCTGAGCCCAGGCCCTCCCTCCCTCAGCCCCCAGTCCCTCCCTCCATCTTCCCTGGGGTTC
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GTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCA
GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG
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GAGCCTGACACTCTCTAAGAGGTTCTCTCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT
TAATTTCTGTCCAACAAACACACACGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG
GTCACTCCTCCTGCCAACATTCAGTCTGGTATGTGAGGCGTGCCTGAAGCAAGAACTCCTGGAGCTACAGGGACA
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GGGAAGGATGTTCTTTTACGTACCAATCTTTTGTCTTTTGATATTAAAAAGAAGTACATGTTTATTGTAGAGA
ATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAA
AA

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